



Qy	91	IANI	94
<b>RESULT</b>			
ID	031938	PRELIMINARY;	PRT;
AC	ACM38	05	168 AA.
DT	01-JAN-1998	(TREMBLrel. 05, Created)	
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)	
DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)	
DE	YONX PROTEIN.		
GN	Bacillus	subtilis.	
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;		
OC	Bacillus/Staphylococcus group; Bacillus.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
STRAIN	-168;		
RX	MEDLINE: 98044013;		
RE	UNP: [REDACTED];		
RA	CUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G., BESSITERES S., BOLOTIN A., BORCHERT S., BRON S., BORRISS R., BOURSIER L., BRAUN M., BRIGNEAU S.C., BRON S., BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARPER N.M., CHOI S.K., CODAN J.J., CONNERON I.F., DEYNE K.M., DUSTERTHOFT A., EHRLICH S.D., ENMERSON P.T., DENITZON F., DEVINE K.M., DUSTERTHOFT A., EHRLICH S.D., ENMERSON P.T., ENTIAN K.D., ERINGTON J., FABRET C., FERRARI E., FOULGER D., FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N., GHIM S.Y., GLASER P., GOFFEAU A., GOILIGHTLY E.J., GRANDI G., GUISEPPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HILBERT H., HOLAPPEN S., HOSONO S., HULLO M.F., ITAYA M., JONES L., JORIS B., KARAMATA D., KASAHARA Y., KLAER-BLANCHARD M., KLEIN C., KOBAYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M., KURITA K., LAPUDIS S., LAUBER J., LAZAREVIC V., LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C., MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M., NOONE D., POHL T.M., PORTETTELL D., PORWOLIK S., PRESCOTT A.M., PARRO V., PUJIC P., PURNELL B., RAPORT G., REY M., REYNOLDS S., PRESECAN E., RIEGER M., RIVOLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F., SATO T., SORIANO A., SOKOWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOKUCHI J., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K., TAKUCHI M., TAMAKOSHI A., TANAKA T., TERESTRA P., TOGNONI A., TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A., VINTAI A., WAMBUUT R., WEDLER H., WETZENGGER T., WINTER P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.; RND: "the complete genome sequence of the gram-positive bacterium Bacillus subtilis"; Nature 390:249-256(1997).		
RA	SEQUENCE FROM N.A.		
RC	[2]		
RL	YONX PROTEIN.		
RT	"the complete genome sequence of the gram-positive bacterium Bacillus subtilis".		
RT	Nature 390:249-256(1997).		
Query	Match	14.6%;	Score 100; DB 2; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENIENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: Z99115; CAB14015.1; -.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 2; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Indels 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENIENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
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Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
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SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
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DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
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SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
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SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW	HYPOTHETICAL PROTEIN.		
SQ	SEQUENCE 168 AA; 19642 MW; 8A3FFB92 CRC32;		
Query	Match	14.6%;	Score 100; DB 9; Length 168;
Best	Local	Similarity 24.1%;	Pred. No. 3.43e-03; Matches 29; Mismatches 32; Indels 5; Gaps 5;
Matches	21;	Conservative	
Db	15	LENENTQYCELDTNLDALKSNRIELESQLEKFESSLTNRQGSIINCRDNLNLGUTH 74	
DR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF020711; AAC13043.1; -.		
KW			

DT	01-FEB-1997	(TREMBLrel. 02, Created)	OS	Cucumis sativus (Cucumber)
DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
DT	01-MAY-1998	(TREMBLrel. 08, Last annotation update)	OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
DE	PENICILLIN-BINDING PROTEIN (FRAGMENT).		OC	core eudicots; Rosidae; eurosids I; Cucurbitaceae;
GN	PBP2X.		OC	Cucumis.
OS	Streptococcus pneumoniae.		RN	[1]
OC	Bacteria; Firmicutes; Bacilli; Clostridium group; Streptococcaceae;		RP	SEQUENCE FROM N.A.
NC	Streptococcus.		RC	TISSUE=FLORAL BUDS;
RN	SEQUENCE FROM N.A.		RL	RC
RC	STRAIN=H12;		RP	Plant Physiol. 116:1192-1192(1998).
RA	REICHMAN P., KOENIG A., MARION A., HAKENBECK R.;		RN	[12]
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.		RP	SEQUENCE FROM N.A.
DR	EMBL: X98366; CAA67012.1; -.		RC	TISSUE=FLORAL BUDS;
PFAM	PF00905; Transpeptidase; 1.		RA	PERL-TREVES R., KAHANA A., KORACH T., KESSLER N.;
FT	NON-TER 1		RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
FT	NON-TER 666 666 AA; 72882 MW; 33B6DC87 CRC32;		DR	EMBL; AF033511; AAC67332.1; -.
SQ	SEQUENCE 666 AA;		MENDEL; 28786; Cucsa; Acc:28786;	
			DR	PFAM; PF00671; Fe_Asc_oxidized; 1.
			SQ	SEQUENCE 282 AA; 31795 MW; 907C682F CRC32;
			RESULT 8	PRELIMINARY; PRT; 314 AA.
			ID	082127
			AC	082127;
			DT	01-NOV-1998 (TREMBLrel. 08, Created)
			DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
			DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)
			DE	ACC_OXIDASE.
			GN	Cucumis sativus (Cucumber)
			OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
			OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
			OC	core eudicots; Rosidae; eurosids I; Cucurbitaceae;
			OC	Cucumis.
			RN	[1]
			RP	SEQUENCE FROM N.A.
			RC	TISSUE=FRUIT;
			RA	SHIMOMI S., YAMAMOTO M., ONO T., KAKUCHI K., NAKAMOTO J.,
			RA	NAKATSUJI A., KUBO Y., NAKAMURA R., INABA A., IMASEKI H.;
			RT	"cDNA Cloning of ACC synthase and ACC oxidase genes in cucumber fruit
			RT	and their differential expression by wounding and auxin.";
			RL	J. Jpn. Soc. Hort. Sci. 67:685-692(1998).
			DR	EMBL; AB006807; BAA33378.1; -.
			DR	MENDEL; 32730; Cucsa; Acc:32730.
			DR	PFAM; PF00671; Fe_Asc_oxidized; 1.
			SQ	SEQUENCE 314 AA; 35470 MW; 640C59E4 CRC32;
			RESULT 9	PRELIMINARY; PRT; 417 AA.
			ID	Q99906
			AC	Q99906;
			DT	01-MAY-1997 (TREMBLrel. 03, Created)
			DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)
			DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)
			DE	DILIC (RHD)
			GN	RHD.
			OS	Homo sapiens (Human).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	PRELIMINARY;	PRT;	667 AA.
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 962650518.			
RA	BECKERS B.A., FAAS B.H., LIGHTRHT P., SIMSEK S., OVERBEEK M.A., DEM BORNE A.E., VAN RHEENEN D.J., DER SCHOT C.E., "Characterization of the hybrid RHD gene leading to the partial D category IIRIC phenotype.", TRANSfusion 36:567-574(1996).			
RN	[2]			
RP	SEQUENCE OF 1-49 FROM N.A.			
RX	MEDLINE; 96420256.			
RA	HUANG C.H.; "Alteration of RH gene structure and expression in human DCCee and DCW red blood cells: phenotypic homozygosity versus genotypic heterozygosity.", BLOOD 88:2326-2333(1996).			
RL	EMBL; SB2449; AAB37696.1; -.			
DR	EMBL; SB3379; CAB34097.1; -.			
DR	PFAM; PF00909; Ammonium_transp; 1.			
FT	NON_TER 417 AA; 45099 MN; BCB058F CRC32;			
SQ	SEQUENCE 417 AA; 45099 MN; BCB058F CRC32;			
Query Match	Best Local Similarity 13.3%; Score 91; DB 4; Length 417; Matches 21; Conservative			
Db	221 PSFNSALLRSPIERKNAVENTYYAVAV-SVVTATGSSLAHPQGKISKTYVHSAVLAGGV 279			
Qy	11 SAIQGSVLTSTCETTINGNTS-SIDLNSVNTDGS-LKWPQSNFIETC-RNTQLAGS 67			
Db	280 AVGTSCHLIPSPWLMVGLVAGLISVGAA-KY 311			
Qy	68 EIAAECKTRAQQFVSTKINLDDHIANIDSTLKY 100			
RESULT	10			
ID	P7228;	PRELIMINARY;	PRT;	666 AA.
AC	P7228;	PRELIMINARY;	PRT;	666 AA.
DT	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	PENICILLIN-BINDING PROTEIN (FRAGMENT).			
GN	PBP2X.			
OS	Streptococcus pneumoniae.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-HU11;			
RA	REICHMAN P., KOENIG A., MARION A., HARENBECK R., "Structure and expression of cDNAs encoding 1-aminocyclopropane-1-carboxylate oxidase homologs isolated from excised mung bean hypocotyls.", Plantae 194:243-249(1994).			
RL	EMBL; X88365; CAA67011.1; -.			
DR	PFAM; PF00905; Transpeptidase; 1.			
FT	NON_TER 1 AA; 666 MN; 0FBAD0A CRC32;			
SQ	SEQUENCE 666 AA; 72761 MN; 0FBAD0A CRC32;			
Query Match	Best Local Similarity 13.2%; Score 90; DB 2; Length 666; Matches 28; Conservative			
Db	88 DASVGEIDFTGPARSYPNGQFQASSFIGAQLENNEDS-KS1LGTGELESSINTILAGT 146			
Qy	10 NAAI1QGSVLTSTCET--NGGYNTS-SIDLNSVNTDGS-LKWPQSNF-IETCRNTQLAGS 66			
Db	147 DGIITYEKDRVGNTVPGT-ELYSQ-QTYDGKDYV 178			
Qy	67 SELAAECKTRAQQFVSTKINLDDHIANIDSTLKY 100			
RESULT	13			
ID	P76052	PRELIMINARY;	PRT;	481 AA.
AC	P76052;	PRELIMINARY;	PRT;	481 AA.
DT	01-FEB-1997 (TREMBLrel. 02, Created)			

DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE FROM BASES 139923 TO 1402712  
 DE (SECTION 121 OF 400) OF THE COMPLETE GENOME (SECTION 121 OF 400).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-12;  
 RX MEDLINE: 97426617.  
 RA BLATTNER F.R., PLUNKETT III G., BLOCH C.A., PERNIA N.T., BURLAND V.,  
 RA RILEY M., COLLADO-VIDES J., GLASNER J.D., RODE C.K., MAYHEW G.F.,  
 RA MAU B., SHAO Y., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,  
 RA "The complete genome sequence of *Escherichia coli* K-12.";  
 RT Science 277:1453-174 (1997).  
 DR EMBL: AE000231; AAC74419; -.  
 SQ SEQUENCE 481 AA; 52133 MW; 8C5C0196 CRC32;  
 SEQUENCE MATCHES 13.0%; Score 89; DB 2; Length 481;  
 Best Local Similarity 30.0%; Pred. No. 2.10e-01;  
 Matches 12; Conservative 12; Mismatches 16; Indels 0; Gaps 0;  
 ORF H0211.

Db 136 GTVFYGCPGEEGSGKTMVREGYFDVDAALTWHPEAF 175  
 QY 15 GSVLTSTCERTGGNTSSIDNSVIENVDGSLKQWPNSN 54

RESULT 14  
 ID 051967 PRELIMINARY;  
 AC 051967;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-1999 (TREMBLrel. 10, Last annotation update)  
 DE ORF H0211.  
 OS Halobacterium sp.  
 OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;  
 OC Halobacterium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 88201675.  
 RA DASSARMA S., DAMERYAL T., JONES J.G., TANDEAU DE MARSAC N.;  
 RT "A plasmid-encoded gas vesicle protein gene in a halophilic  
 archaeobacterium.";  
 RA Mol. Microbiol. 1:365-370(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 90016863.  
 RA JONES J.G., HACKETT N.R., HALLADAY J.T., SCOTHORN D.J., YANG C.F.,  
 RA NG W.L., DASSARMA S.;  
 RT "Analysis of insertion mutants reveals two new genes in the pNR1C10  
 gas vesicle gene cluster of *Halobacterium halobium*.";  
 RA Nucleic Acids Res. 17:7785-7793(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 91267967.  
 RA NG W.L., KOTHAKOTA S., DASSARMA S.;  
 RT "Structure of the gas vesicle plasmid in *Halobacterium halobium*  
 inversion isomers, inverted repeats, and insertion sequences.";  
 RA J. Bacteriol. 173:3933-3933(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 91323716.  
 RA JONES J.G., YOUNG D.C., DASSARMA S.;  
 RT "Structure and organization of the gas vesicle gene cluster on the  
 Halobacterium halobium plasmid pNR1C100.";  
 RA Gene 102:117-122(1991).

[5] SEQUENCE FROM N.A.  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 93012964.  
 RA HALLADAY J.T., JONES J.G., LIN F., MACDONALD A.B., DASSARMA S.;  
 RT "Genetic transformation of a halophilic archaebacterium with a gas  
 vesicle gene cluster restores its ability to float.";  
 RT RL Gene 119:131-136(1992).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 93139036.  
 RA HALLADAY J.T., JONES J.G., LIN F., MACDONALD A.B., DASSARMA S.;  
 RT "The rightward gas vesicle operon in *Halobacterium* plasmid pNR1C100:  
 identification of the gvpA and gvpC gene products by use of antibody  
 probes and genetic analysis of the region downstream of gvpC.";  
 RT RL J. Bacteriol. 175:684-692(1993).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 93327890.  
 RA DASSARMA S.;  
 RT "Identification and analysis of the gas vesicle gene cluster on an  
 unstable plasmid of *Halobacterium halobium*.";  
 RT RL Experientia 49:482-486(1993).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 93338662.  
 RA DASSARMA S.;  
 RT "Minimal replication origin of the 200-kilobase *Halobacterium* Plasmid  
 pNR1C100.";  
 RT RL J. Bacteriol. 175:4584-4596(1993).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RX MEDLINE: 9505934.  
 RA DASSARMA S., ARORA P., LIN F., MOLINARI E., YIN L.R.;  
 RT "Wild-type gas vesicle formation requires at least two genes in the  
 gvp gene cluster of *Halobacterium halobium* plasmid pNR1C100.";  
 RT RL J. Bacteriol. 176:7646-7652(1994).  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RA NG W.L., ARORA P., DASSARMA S.;  
 RL Syst. Appl. Microbiol. 16:560-568(1994).  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RA DASSARMA S.;  
 RL (ID) RODD F.T., PLACE A.R., SOWERS K.R., SCHREIER H.J., DASSARMA S.,  
 RL FLEISCHMANN E.M. (eds.);  
 RL Archaea:  
 RL A laboratory manual - halophiles, pp.253-255,  
 RL Cold Spring Harbor Laboratory Press, New York (1995).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RA DASSARMA S.;  
 RL (ID) RODD F.T., PLACE A.R., SOWERS K.R., SCHREIER H.J., DASSARMA S.,  
 RL FLEISCHMANN E.M. (eds.);  
 RL FEMS Microbiol. Lett. 153:1-10(1997).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NRC-1;  
 RA NG W.L., CIUFO S.A., SMITH T.M., BUMGARNER R.E., LORETT C., BASKIN D.,  
 RA FAUST J., SETO J., SLAGEL J., HOOD L., DASSARMA S.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF016485; AAC82797.1; -.

DR PFAM: PF00096; zf-C2H2; 1.  
 KW Plasmid.  
 SQ SEQUENCE 202 AA; 23627 MW; 2DEB3572 CRC32;

Query Match 12.9%; Score 88; DB 1; Length 202;  
 Best Local Similarity 35.3%; Pred. No. 3.01e-01;  
 Matches 12; Conservative 12; Mismatches 9; Indels 1; Gaps 1;  
 Job time : 17 secs.

Db 160 ATTCRISGAHE-NSIDTSPVSETIDGDSWRSS 192  
 Qy 19 TSTCERTGGYNTSSIDLNSVENVGSLKQPS 52

RESULT 15

ID 054474 PRELIMINARY; PRT; 666 AA.

AC 054474;

DT 01-NOV-1996 (T-EMBLrel. 01; Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01; Last annotation update)  
 DT 01-NOV-1998 (T-EMBLrel. 08; Last annotation update)

DR PENICILLIN BINDING PROTEIN (FRAGMENT).

GGPBPX.

OS Streptococcus mitis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

OC Streptococcus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-1012;

RX MEDLINE; 95020605.

RA SIBOLD C., HENRICHSEN J., KOENIG A., MARTIN C., CHALKLEY L.,  
 RA HAKENBECK R.;

RT "Mosaic pbpx genes of major clones of penicillin-resistant  
 Streptococcus pneumoniae have evolved from pbpx genes of a penicillin-  
 sensitive Streptococcus oralis."

RT Mol. Microbiol. 12:1013-1023 (1994).

EMBL; X78216; CAA55061.1;

DR PFAM; PF00905; Transpeptidase; 1.

FT NON-TER 1

FT 666 666

SO SEQUENCE 666 AA; 72906 MW; FD424A39 CRC32;

Query Match 12.9%; Score 88; DB 2; Length 666;  
 Best Local Similarity 25.6%; Pred. No. 3.01e-01;  
 Matches 22; Conservative 26; Mismatches 36; Indels 2; Gaps 1;

Db 88 DASVSEGIDFTSPNRSYPNQGAFASSEFIGLAQHENEEDGSKSLIGTSGLESSINTLAGTD 147  
 Qy 10 NSAIQGSVLSTCERT--NGGYNTSSIDLNSVENVGSLKQPSNFETICRNTQLAGSS 67

DI 148 GIITYEKDRVGNIVPGTEQVSSQTVD 173

Qy 68 EIAAECKTRQQFVYSTKINLDDHIAN 93

Search completed: Wed Aug 16 09:45:47 2000  
 Job time : 17 secs.